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Review

# Harnessing the Power of Genomics to Secure the Future of Seafood

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**Best use of scientific knowledge is required to maintain the fundamental role of seafood in human nutrition. While it is acknowledged that genomic-based methods allow the collection of powerful data, their value to inform fisheries management, aquaculture, and biosecurity applications remains underestimated. We review genomic applications of relevance to the sustainable management of seafood resources, illustrate the benefits of, and identify barriers to their integration. We conclude that the value of genomic information towards securing the future of seafood does not need to be further demonstrated. Instead, we need immediate efforts to remove structural roadblocks and focus on ways that support integration of genomic-informed methods into management and production practices. We propose solutions to pave the way forward.**

## Pressing Need for Best Science Practices to Secure the Future of Seafood

Seafood plays a fundamental role in meeting current and future food needs [1]. Capture fisheries use the only remaining wild animal protein source, and aquaculture is the fastest growing food production sector in the world. Together they provide 4.5 billion people with at least 15% of their animal protein [2,3]. The human population may exceed 9 billion by 2050, so a pressing question is whether fisheries and aquaculture can help to alleviate food security issues [3]. The answer to this remains unknown. Seafood needs of some developed countries can no longer be sustained from local fish stocks and are increasingly supplemented from elsewhere [4]. This trend will probably remain or increase over time, as several stocks are near or above sustainable limits [5,6], and many fisheries remain overexploited or near collapse [4,7,8]. For example, 95% of fish stocks in the Mediterranean and Black Seas are overharvested [8]. Fisheries are also being severely affected worldwide by the cumulative effects of habitat degradation, climate change,and diseases [39]. While finfish production from aquaculture has reached the volume of wild fisheries [10], growth is expected to decelerate in response to freshwater shortage, lack of suitable locations, and increasing feed costs [11]. Moreover, other aquaculture industries (e.g., shellfish) are suffering production setbacks due to disease outbreaks and ocean acidification [12].

### Trends

Advancements of genetic technologies now allow the collection of genome-wide data in nonmodel species in a cost-effective manner.

These genomic-informed technologies allow addressing a comprehensive spectrum of needs and applications relevant to fisheries, aquaculture, and biosecurity.

Genomics tools also improve our understanding of how aquatic organisms adapt and respond to the environment, and improve our ability to monitor environmental variation and exploited species.

Genomic approaches are now rapidly replacing traditional genetic markers, but their application in fisheries and aquaculture management has stagnated when compared to agriculture where they have long been used for improved production.

There is no reason to further delay the application of genomic tools in fisheries management and aquaculture production.

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Careful management and production strategies are required to maintain a sustainable future for the seafood industry, making it critical that the best scientific knowledge informs decision-making [3,4,13]. Traditional scientific fisheries management relies on stock assessment models to predict variability in stock–recruitment relationships to determine sustainable catch limits [7,14,15]. Genetic methods can also provide fundamental data to inform fisheries management and aquaculture production [16], however, the integration of genetic data has stagnated (Box 1). Consequently, and despite the demonstrated ability of genetic data to delineate populations accurately (see section below), management units are predominantly based on administrative units, which are often not closely connected with population biology [8,17]. This contradicts the basis of fisheries science whereby the Maximum Sustainable Yield (MSY) can only be achieved by the efficient management of distinct populations [8,16,18].

## Genetic and Genomic Applications Can Help Secure the future of Seafood

Novel technologies now allow the collection of genome-wide data to better inform fisheries management, biosecurity, and aquaculture applications [19,20]. Genomic approaches are now rapidly replacing traditional genetic markers (e.g., microsatellite DNA), but as with genetic data, little is used when developing management policies (Box 1). Genomics refers to approaches relating to the complete genome of an organism [21]. In population genetics, the term genomics

### Box 1. Why Genetic Data Has Seldom Been Incorporated into Fisheries Management, and What to Do about it

The fisheries genetics explosion began in the 1980s propelled by the allelic interpretation of the electrophoretic mobility of proteins and accelerated now by the genomics revolution 9Snapper9 [49]. Sadly, exclamations of the practical value of population genetics for management and conservation have largely fallen on deaf ears. Despite trouble-shooting by experts [16,50], impediments to the downstream use of genetics in seafood production still remain.

To systematically address this, three user groups were consulted in one-to-one structured interviews [51]. The groups were fisheries scientists ($n$ = 26), fisheries managers ($n$ = 24), and fishing industry representatives ($n$ = 12) in Australia, Europe, North and South America, Western Pacific, South Africa, and New Zealand. The purpose was to qualitatively assess attitudes and perceptions on the use of genetics in a fisheries management context to determine if there were barriers to the uptake of genetic information and how this might be improved. Over 90% of interviewees were familiar with the use of genetics for fisheries stock structure (Theme II in [52]). The awareness of the remaining ten genetic themes was poor to moderate. Industry and management representatives viewed the role of genetics in fisheries more positively than fisheries scientists. The basis for positive attitudes was the recognition of the general usefulness of genetics, in particular for defining the spatial structure of populations. Where there was a negative perception by interviewees, several reasons were provided:

- A general lack of understanding of the potential value of genetic information,
- A perception that genetic studies are expensive,
- A perception that genetic results are often 'oversold',
- A lack of consistency in interpretations of results by geneticists,
- The importance of genetic information was far outweighed by other inputs to management decisions.

All interviewees agreed that the role and effectiveness of genetic information in fisheries management could be improved. The suggestions were grouped into two categories: communication and technical. Improvements to communication strategies (around 70% of suggestions) were considered essential. Specific suggestions included: improved communication of results across user groups using plain language; greater communication among fishery scientists, geneticists, fishery managers, and industry; a need for greater understanding of the utility of genetic methods by user groups; and greater accessibility to genetic research and geneticists. Technical suggestions for improvement included reducing cost of genetic projects; more robust and reliable genetic techniques; and more robust sampling designs.

Unhappily, communication challenges are still a roadblock for the uptake of genetic data, which is a wake-up call for those involved in genomics for seafood security. There are glimmers of hope that attitudes are changing. The survey showed that most understand its power for defining fisheries stocks and are sympathetic, if not knowledgeable, about the role of genetics. Thus, the judicious use of genomics is likely to be well received, but its application needs to be carefully tailored to provide solutions for management and policy issues (Ovenden and Moore, S11). The onus is on geneticists and end-users to reach mutual understanding (Figure I), or else the improvement in the perceived value of genetics to the seafood industry will be not be sustained.

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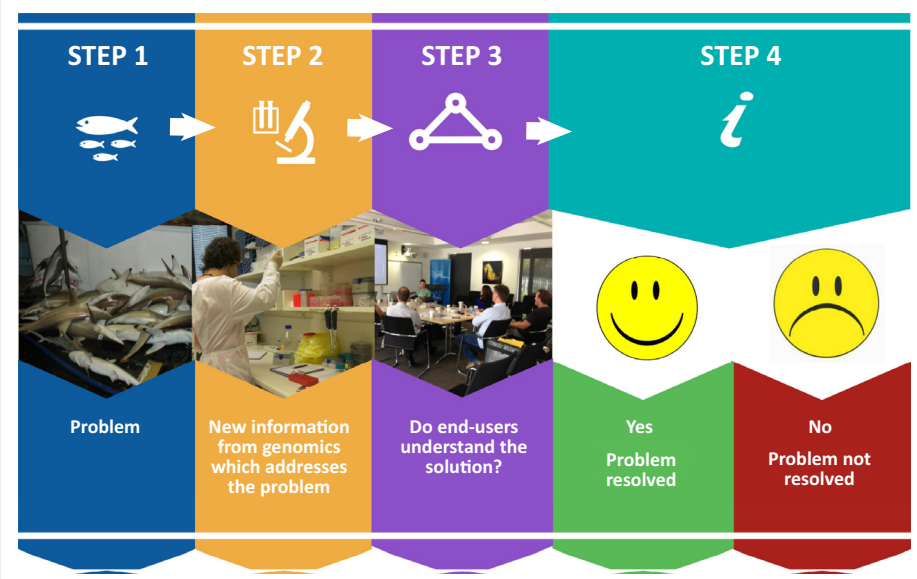


Figure I. The purpose of this simple diagram is to emphasise that unless the solutions provided by genomics are not made clear to stakeholders, then the problem is not solved. Even if geneticists believe the problem is solved with new information deduced from genomics, end-users such as fisheries scientists, managers, and representatives need to understand and accept the solution also. The diagram leaves out important steps such as integration with other data sources or follows on actions for further problem solving or implementation.

is typically used as a shorthand to describe studies applying large and genome-wide datasets; with a typical, yet arbitrary, threshold of >1000s versus 10s–100s of markers to distinguish between genomic and genetic studies, respectively. For decades, only low-resolution genetic methods were available to address issues pertaining to fisheries management and aquaculture. Indeed the first genome sequence of a key seafood production species was published in 2011 [22].

While the limited incorporation of genetic information into fisheries and aquaculture management is not a new problem [16], genomics makes the situation qualitatively different. This is because genomic-informed technologies allow for the first time the development and application of cost-effective genetic tools that can address a comprehensive spectrum of needs and applications relevant to fisheries and aquaculture management, biosecurity, and traceability in the supply chain [23] (Figure 1). Specifically for fisheries management, genomics defines management units, quantifies the extent of adaptive divergence and connectivity between them, and allows performing mixed-stock analysis with substantially increased resolution. Genomic tools also have the potential to advance aquaculture production by means of genomic selection for growth or disease resistance, and identifying wild populations with the greatest potential for domestication [24]. Genomics can also increase biosecurity, for example, by identifying escapees from fish farms. A small to moderate number of markers may sometimes provide sufficient power to address the question at hand [19,25], yet genomic-informed approaches often provide a necessary first step for identifying the best set of markers to be used in subsequent surveys. Tools derived from genomics can also improve our understanding of how aquatic organisms adapt and respond to their environments from the species

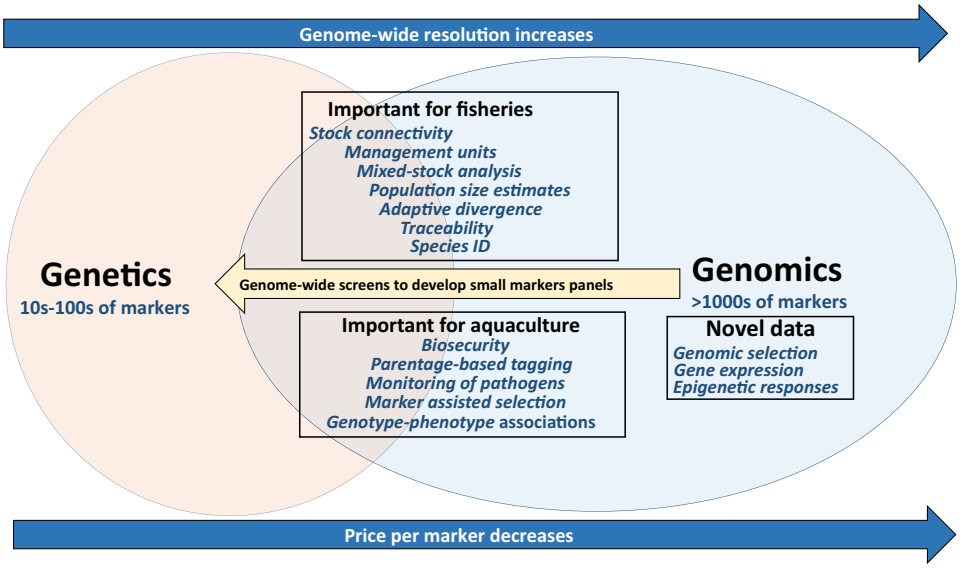


Figure 1. Genetics versus Genomics. Applications are italicised. Applications placed within the overlap area between genetics and genomics can be conducted with both methods, but always achieve finer resolution using genomic technologies. Some applications potentially relevant to either fisheries or aquaculture are only possible with genomic methods, and include 'genomic selection', 'gene expression', and 'epigenetic responses'. Some applications are particular important (but not exclusively) for either fisheries or aquaculture. The ability to screen for genome wide single nucleotide polymorphism markers and then to develop small markers panels most powerful for the questions at hand (e.g., species or ecotype identification, stock structure, parentage-based analysis, and mixed-stocks analysis) is only possible with the use of genomic technologies. The price for typing a few 10–100s of markers compared to 1000s of markers decreases on a per marker basis.

to the community level, and improve our ability to monitor biological environmental variation or exploited species, for instance, as provided by the exponential development of environmental DNA (eDNA) and metabarcoding methods [26].

## Examples of Genomics Applications from around the Globe

The following outlines representative examples of genomic applications of direct relevance to fisheries management, aquaculture, and the conservation of exploited species, as well as for food quality and safety purposes. Details for each of these case studies are presented in 14 short papers (S1–S14) in the Supplementary Material that summarise the presentations of invited speakers during a symposium entitled: "Genomics for improved fisheries management and conservation: have the promises been fulfilled?"

Accurate identification of fisheries management units and species is mandatory to enable proactive population management. Bernatchez (S6) reported how using several thousands of single nucleotide polymorphism (SNP) markers allowed the refinement of management units of the American lobster, documenting the degree of overlap between biological and current management units, while also providing evidence for local adaptation. Regional patterns of recruitment in the American eel are affected by selection imposed by the local environment, which has been shown to recur in every generation following dispersal from a single spawning area (Bernatchez, S6). This finding may influence both global and local restoration strategies. Species identification for improved conservation practices can also be aided by genomic-based approaches. For example, Lee *et al*. (S7) showed that adaptive and neutral markers have considerable potential to discriminate cryptic species of sympatric freshwater fishes on the

Korean peninsula. Similarly, Araneda and Larraín (S1) demonstrated the usefulness of a moderate number of markers derived from genomic methods for the management and traceability of seafood species (Box 2).

Many marine species are widely distributed in space, and vulnerable populations may intermingle with abundant ones during parts of their life history, meaning that accurate forecasting in fisheries management relies on identifying source or parent populations. One such example comes from Barth and colleagues (S4 and Box 2) on North Atlantic cod stocks composed of different ecotypes, where they identified distinct chromosomal rearrangements associated with life-history traits. A few markers linked to these polymorphisms enable ecotypes to be distinguished, which facilitates appropriate harvest strategies on variant ecotypes during different seasons. Work on Pacific salmon on the West Coast of North America showed that physical tagging can be replaced by genetic tags [27]. Parentage-based tagging (PBT) allows accurate estimates of the contribution of hatcheries to local recruitment in commercially and culturally important Coho Salmon populations off British Columbia, Canada (Beacham *et al.*, S5). The wide distribution of migratory fish stocks also holds particular challenges for the treatment of emerging diseases. Here, Miller (S10, and Box 3) showed how a gene expression assay developed from genomic technologies can simultaneously provide rapid diagnosis of multiple pathogens.

Population-based approaches also extend to the management of hybrids. Naturally occurring hybrid taxa warrant protection [28], but detecting hybrids can be limited, with few markers. Thousands of SNPs were used to identify different classes of hybrids between two co-occurring Blacktip Shark species in Australia (Maes *et al.*, S8), providing tools to assess

## Box 2. Genomic Approaches for Seafood Traceability

Traceability of marine or aquacultured products like finfish and shellfish throughout the food chain ('from the ocean to the fork') with high certainty about their origin and identity is crucial for their sustainable utilisation, the conservation of exploited stocks, and to prevent food fraud [53]. In general, species and their origin may be identified by external traits; however, phenotypic tracing becomes unusable once the species has entered food processing. Genetics and genomics resources provide powerful tools, with high reproducibility and reliability, for tracing and identifying marine products; they can easily be combined and compared with reference materials [54] to determine authenticity, and to verify labelling information. Traceability can be applied on three broad levels: species, population, and individual identification. Hitherto, the first two levels have been explored using either genetics or genomics derived methods.

Two objectives of the species level include preventing food fraud by the substitution of a valuable species with lower value species and marketing of potentially harmful to the consumer or protected species [55–58]. Many examples of mislabelling have been detected through analysis of the cytochrome oxidase I gene (COI) and by comparing this with the database of DNA barcoding (FISH-BOL) [59–61]. DNA barcoding is less developed in shellfish because species identification often requires the development and applications of different mitochondrial and nuclear molecular markers as well as SNP panels [62] depending on taxa [63]. Examples include, separation of Mediterranean mussel, common blue mussel, Baltic mussel, and Chilean mussel with high accuracy using a panel of 49 SNPs (Larraín et al. in preparation) and the separation of Chilean and Mediterranean mussels with a subpanel of 19 SNPs (Araneda and Larraín, S1).

The objectives for the second (population) level include preventing the sale of products from illegal, unreported, and unregulated fisheries, and protecting consumers from seafood products collected in areas affected by threats to public health (for example, harmful algal blooms). Assignments based on a moderate number of non-neutral SNP markers identified using genomics have been successful at differentiating among fish species (Atlantic cod, Atlantic herring, sole, and European hake) from different geographical areas in Europe [31]. In Chilean mussel, this approach allowed to differentiate populations from three different environments [64], two of which were affected by the red tide in 2016, thus permitting physical traceability (records, labels). Such small panels of informative SNPs usually perform better than microsatellite markers when allocating individuals to geographic origin [65]. Within ecologically, but not geographically differentiated populations characterized by high gene flow, such as Atlantic cod in the Eastern North Atlantic, North Sea, and Baltic Sea (Figure IA), adaptive variation may manifest only in a few genomic regions (e.g. chromosomal inversions), illustrating the importance of genome-wide tools for tractability (Figure IB) [66–70, Barth S4].

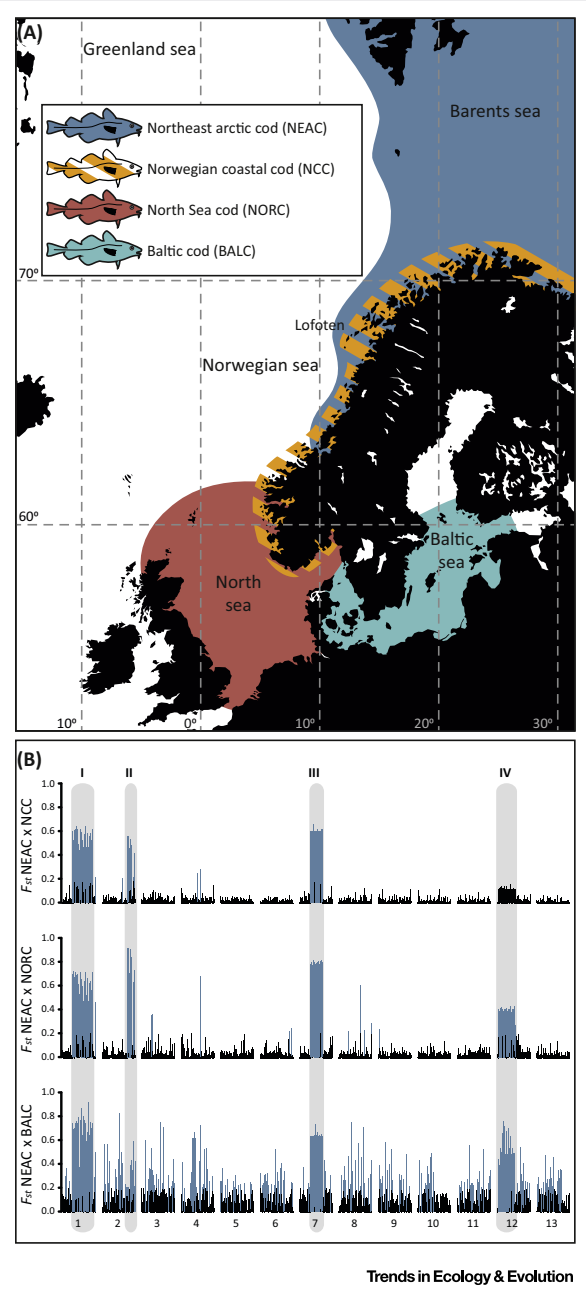


Figure I. (A) Geographic distribution of Atlantic cod ecotypes in the Northeast Atlantic. (B) Pairwise differentiation ($F_{ST}$) between ecotypes illustrates the low genome-wide divergence. Four regions (I–IV, gray outline on chromosomes 1, 2, 7, and 12) show high $F_{ST}$ and correspond to chromosomal rearrangements that likely play a role in ecological adaptation [66–69, Barth S4].

the population status of harvested sharks accurately. In contrast, the outcomes of anthropogenic hybridisation warrant close monitoring. On the West Coast of North America, hatchery salmon, which are reproductively segregated from their wild counterparts are released to minimise harvest of wild populations [29]. However, extensive genetic-based surveys in

Canada have revealed widespread straying of released salmon, accompanied by introgression affecting the structure of wild populations (Withler *et al*., S14). In contrast, deliberate hybridisation may be used to restore small and wild populations to minimise genetic divergence between cultured individuals and their wild conspecifics. Waters *et al*. (S13) compared the rate of genome-wide change in hatchery individuals that are reproductively integrated with wild populations, to hatchery fish that are reproductively segregated. The reduced rate of change in the integrated population has provided insights into the genetic benefits and risks associated with contrasting captive breeding approaches. Genomic approaches can also provide insight into the adaptive spatial and temporal population structuring of species, as well as into their molecular basis (Box 4). Therkildsen (S12) demonstrated the power of genomics towards elucidating the genomic basis of rapid fisheries-induced evolution causing changes in growth rate and age at reproduction, which may affect the productivity of fisheries. Barson *et al*. (S3) combined the uses of a SNP array and whole-genome resequencing of Atlantic salmon to identify genome regions that have large effects on such life-history traits, and subsequently used a few markers from key genes to derive recommendations for conservation and management [30]. Finally, Ashton *et al*. (S2) showed the value of an integrative genomics-informed approach in the aquaculture production of a newly domesticated species, and demonstrated how genomic approaches facilitate the design of selective breeding programmes to develop new cultivars adapted to different environmental conditions and production mode.

### Box 3. Detection of Seafood Diseases Using Genomics: Heart and Skeletal Muscle Inflammation (HSMI) as an Example

The role of infectious diseases in wild Pacific salmon has declined and the potential risk that the Atlantic salmon farming industry poses to the transmission of infectious agents has been a topic of high scientific, public, and political concern in British Columbia (BC), Canada, where there is a growing aquaculture industry and still abundant, but declining wild stocks. A salmon health project undertaken to characterise the infectious agents and diseases impacting salmon in BC was developed; this project applied novel genomic technologies together with traditional fish health diagnostic approaches to provide scientific data and advice on these issues [71].

An early study identified a previously undiagnosed disease, HSMI, highly prevalent on a BC salmon farm [72]; this disease has greatly affected the Norwegian salmon farming industry but was not known to exist outside of Europe and Chile [73]. Evidence from Norway suggests that HSMI is caused by the piscine ortho-reovirus (PRV) [74]. In the BC study, an assessment of infectious agents was undertaken using a microfluidics-based quantitative PCR platform developed using high throughput genomic technologies (Miller, S10; Figure I), and showed that PRV was the only agent statistically associated with the disease and colocalised in the area of tissue damage. Next-generation sequencing identified the full PRV genome sequence and verified that no other viruses were associated with the disease. Whereas PRV was known to be present in BC [75], the BC farm veterinary community and fish health scientists believed that the disease, HSMI, was not [76] and that the BC variant of the virus was avirulent [77,78]. Moreover, there was an ongoing Federal Court case in which the environmental law organisation Ecojustice sued Fisheries and Oceans Canada (DFO) (and Marine Harvest Canada) for unlawful delegation of their regulatory responsibilities to industry and insufficient protection of wild fish from harmful diseases or disease agents ( http://www.mandellpinder.com/alexandra-morton-v-minister-of-fisheries-and-oceans-and-marine-harvest-canada-inc-2015-fc-575-case-summary/). This suit was based on the fact that a set of hatchery fish that tested positive for PRV was allowed to be transferred to ocean farms; the plaintiff argued that this constituted transfer of diseased fish, contrary to the Fisheries General Regulations. The defendants contended that expert advisors indicated there was no evidence of HSMI in BC and insufficient evidence to prove that PRV caused HSMI. The judge ruled in favour of the plaintiff on the basis that the precautionary principle, which reasons that lack of complete scientific certainty should not be used as a basis to avoid or postpone protecting the environment, was not properly applied by the industry regulator, DFO. Lawyers for both defendants appealed this decision, but upon being informed of the new results, DFO called a press release (http://news.gc.ca/web/article-en.do?nid=1069579&_ga=2.230101532.1890423932.1495143055-1102475227.1480282937) and both defendants dropped their appeals. Given that the judgement required the regulator to strengthen the conditions of the license to better reflect the standards of the Fisheries General Regulations, the research will, in the future, impact governance over the Aquaculture Industry.

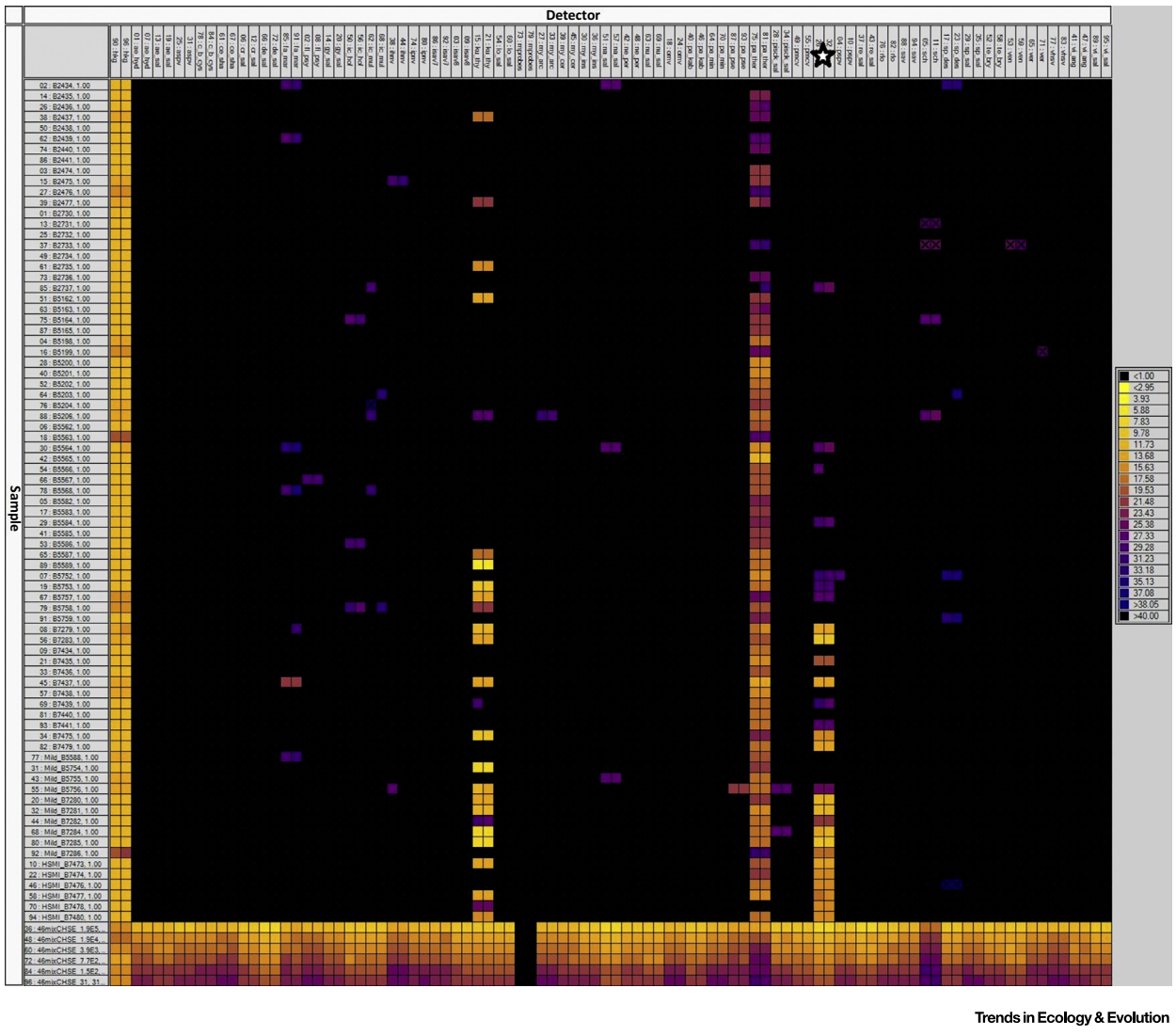


Figure I. Heatmap from the Fluidigm Biomark Microfluidics Infectious Agent Monitoring Platform Depicting Detections for 45 agents from the Farm Study. Duplicate assays of the 45 agents are on the x axis, individual samples on the y axis (HSMI positive fish above positive controls at base), and PRV is starred.

## Current State of Fisheries Governance, Management and Policy Making, and the Potential Roles for Genomics

In fisheries resource management, the most common use of genetic data has been the delineation of the spatial extent and structure of populations [16]. New applications are developing rapidly, such as underpinning efforts to maintain biodiversity and curb illegal, unreported, and unregulated fishing [31] and food fraud [32]. Here, the contribution of DNA analysis to Pacific salmon fisheries management has been exemplary, providing a striking example of the benefits that result from considering genetic/genomic information. Genetic stock identification (GSI) has been incorporated into management activities for the past 35 years [18,33], progressing from allozymes to microsatellite loci [34] and now to SNPs

Box 4. Adaptive Variation and Fisheries Induced Evolution: New Insights from Genomics

Mounting evidence suggests that fishing pressure has caused substantial life history changes in many commercial fish stocks [79,80]. These changes (e.g., slower growth rates and/or earlier maturation) are of concern because they may reduce stock productivity and resilience to overfishing. Although most recorded shifts appear at least partially genetic, it has been difficult to disentangle environmental, ecological, and genetic effects fully because the available evidence primarily builds on observations from natural populations [81,82]. Accordingly, there is ongoing controversy about whether fishing practices actually drive genetic changes in the exploited populations and hence if the evolutionary impacts of exploitation should be considered part of sustainable fisheries management.

Genomic tools are able to shed new light on this issue. Temporal sampling of wild fish stocks has already provided the first DNA-level evidence of fisheries-induced evolution, either through scans of candidate genes [83,84], or larger panels of markers [85,86]. However, spatiotemporal population complexity and difficulty filtering out the effect of fishing from other drivers of selection, for example, climate change, have limited the conclusiveness of these studies (Therkildsen, S12). Experimental studies have provided more robust evidence of particular genes being affected by fisheries-induced selection [87,88], sometimes in great numbers [89], and our ability now to screen the entire genomes of nonmodel organisms makes it possible to expand on these findings for a more comprehensive understanding of the general nature of genomic changes fisheries selection is likely to induce. For example, does it tend to occur through large allele frequency changes in a few genes or smaller changes in many genes? Does evolutionary change occur through changes in protein-coding sequence or in gene expression? Are particular genes or physiological pathways consistently targeted? How extensively does selection erode diversity throughout the genome? Such knowledge is critical for enabling accurate modelling of future stock abundances under size-selective harvesting.

It is generally assumed that life history traits are highly polygenic, that is, based on small effects from many loci [90,91]. Consequently, most current models of fisheries induced evolution make this assumption [92]. Several recent studies, using genomic methods, however, have revealed single genes explaining high proportions (39–46%) of phenotypic variation in key traits in wild fish populations [93,94] and modelling of selection responses to fishing has recently been shown to be highly dependent on the trait architecture [92]. Thus, a better understanding of links between genotype and life-history phenotypes, enabled by genomics, can be of great benefit for accurately modelling sustainable yields in fisheries-targeted species.

[35,36, Beacham *et al*. S5]. Genetic studies have also supported the regulation of hatchery programmes for wild fisheries [37] (Waters *et al*. S13, Withler *et al*. S14). The long, seamless history of DNA analysis that underpins the management of Pacific salmon is a consequence of the high socioeconomic value of this fishery, open-minded collaborations between managers, fishery scientists, and geneticists, and a solid analytical infrastructure in government and academic institutions. Other successful examples include cooperative studies that generated useful information for rapid inclusion in management (Ovenden and Moore, S11). Some applications have developed from serendipitous discoveries, such as use of the *Pan*I locus to manage the mixed-stock fishery for Northeast Arctic and coastal Atlantic cod off Norway [38]. There are also examples in which genetics/genomics support marine fisheries management [38]. In some cases, such as the EU Common Fisheries Policy (CFP), acute policy needs have driven the accommodation of genetics (Martinsohn S9, Box 5). Once the basic biology of a species is known, the usefulness of genetic/genomic information increases rapidly as management regimes develop, including applications such as genetic species identification [39,40].

## Genomic Data and Policy Decisions: Causes of Lack of Integration

Many factors constitute impediments to the stronger integration of genetics and genomics into fisheries and aquaculture policy and management. Wild fisheries take place in complex and diverse ecosystems. For example, in Australia and New Zealand, management encompasses a diversity of species occurring in temperate to tropical environments (aquaculture). The majority of these fisheries are marine and are exploited sustainably [41], and collectively, and they are worth billions of dollars. In contrast, overexploitation is an issue in Europe [42], and fisheries as well as aquaculture in many coastal communities carry considerable socioeconomic significance [16]. This setting illustrates the intricate aggregate of social, cultural,

### Box 5. EU CFP: Cherishing Scientific Advice while Neglecting Genetics and Genomics

The CFP is a major policy framework underpinning EU fisheries and aquaculture management. Under the CFP, 28 EU Member States share the management of the common natural renewable resource of fish and shellfish. The CFP aims to ensure that fisheries and aquaculture are sources of healthy, environmentally, economically, and socially sustainable food [95].

Worldwide legislation and policy frameworks for aquatic resources point towards the importance of scientific information (Figure I); a notion also legally endorsed by the CFP (102): to enable the provision of best available scientific advice, the CFP obliges EU Member States to collect biological, catch, effort, and economic data [96]. The creation and provision of scientific advice is ensured through data collection schemes and dedicated scientific advisory bodies such as the Scientific, Technical and Economic, Committee for Fisheries (STECF) and the International Council for the Exploration of the Sea (ICES). Such data are then analysed by the STECF [97] and ICES working groups. Other advisory bodies also play a role [98]. Support for research relevant to the CFP is available, for example, through the EU Framework Programme Horizon 2020 and the European Maritime and Fisheries Fund [99]. The CFP provides a fertile environment to integrate scientific advice into its policy cycle, as shown by the high number of references to STECF in EU legislation: the official EU law website lists 21 legislative acts with reference to STECF for 2016 [100]. Remarkably, EU law explicitly refers to genetics for fisheries control (Martinsohn, S9). It is thus disappointing that genetics and genomics incorporation in scientific advice under the CFP remains marginal. Of the ~400 scientists involved in STECF, none is a geneticist and none of the 20+ STECF Expert Groups convened annually relates to genetics.

The reasons for this missed opportunity are manifold and outlined in the "Ways Forward" section and in Martinsohn (S9). One factor is that the CFP sets distinct targets, such as fishing at MSY by 2020 [95]. Such targets are currently primarily tackled by traditional fisheries science, involving institutions and experts that have supported CFP advice for decades, and which are embedded in an infrastructure tailored to support fisheries and aquaculture management and policy. Fisheries and, albeit less so, aquaculture-relevant genetic research is largely restricted to academia and is driven by the quest for cutting edge knowledge and the desire to publish. As a result, CFP requirements and collaboration with other fisheries scientific fields and stakeholders are neglected. Nevertheless, it is promising that STECF has recently referred more frequently to genetics [38] and that examples for the successful integration of genetic and genomic information into fisheries management and cooperation with the fishing and aquaculture industry accumulate (Martinsohn, S9).

| | USA | Canada | Australia | European Union |
|---|---|---|---|---|
| Legal framework | Magnuson–stevens fishery conservation and management act | Fisheries act R.S.C., 1985, c. F-14 Coastal fisheries protection act | Australian fisheries management act | Common fisheries policy |
| Objectives | • Conservation; rebuilding; employment<br>• Food;<br>• Revenue. | • Sustainable aquatic ecosystems;<br>• Economic prosperity. | • Sustainable fisheries;<br>• Net economic return. | • Fishing/aquaculture environmentally, economically and socially sustainable;<br>• Source of healthy food for EU citizens;<br>• Profitable. |
| Scientific support endorsed | SEC.2. Findings, purposes, and policy 101-627, 104-297 | e.g. Agreements, programs and projects [4.1] | Indirectly referred to [3a] | Regulation (EU) 1380/2013 (multiple articles) |

Trends in Ecology & Evolution

Figure I. An International Comparison of Scientific Advice Feeding into Fisheries Management Using the USA, Canada, Australia, and EU.

economic, and environmental conditions surrounding fisheries and aquaculture regulation. The development of sound seafood policy is further complicated by jurisdiction over public

land and fishing grounds. For instance, under the CFP, all 28 EU Member States share access to fish stocks in addition to agreements with neighbouring nations that are not EU Member States (Box 5). Regional governance might further complicate national policy developments. For example, ownership can be claimed at the village, county, or state level in Japan [43]. Jurisdiction tends to be simpler for single nations like Australia, where the exclusive economic zone (EEZ) is contiguous with those of its neighbours for <10% of its total length.

Despite DNA providing a significant range of information relevant to fisheries and aquaculture [25], it is only one aspect of the knowledge needed for policymaking. Some harvested species around the world are not well described scientifically, resulting in projects prioritising the collection of basic biological information about a species over DNA studies. This is particularly true for small artisanal multispecies fisheries in developing countries that struggle with different and more basic problems, but are no less important for seafood production. Furthermore, training of fisheries scientists has traditionally focussed on teaching aquatic ecology, population dynamics, and catch quota management. This partially explains the persistent lack of DNA data alongside other traditional biological fisheries data, such as length at catch, age, and sex for fisheries management purposes.

## Ways Forward

Given the fundamental role that seafood plays in consolidating food security and considering all the sizable challenges that need to be overcome to secure its sustainability, it is imperative that the best scientific knowledge is put into practice. This paper adds to previous voices that DNA-based methods have much to offer to inform seafood management and aquaculture practices, but their application has stagnated [16,19] when compared to say, agriculture, where genetic/genomic data has long been used in the development of breeding schemes and improved production [44]. Our case studies illustrate the benefits that can be gained from genomics, and the evidence emerging from such studies reveals several key applications that may be performed more efficiently than using traditional genetic markers. First, scaling up genome coverage for nonmodel species leads to refined estimates of population genetic parameters, especially in the many marine species that are weakly structured. Second, it is possible to identify genetic markers that better facilitate the definition of management units based on adaptive criteria as well as the development of diagnostic markers for managing the spread of pathogens or invasive species. Third, new, simple and affordable methods derived from genomics allow improved genetic tagging to identify the species or the population of origin of exploited fish, as well as their associated pathogens. These methods also allow estimating real-time migration rates and dispersal, thus informing strategies for sustainable exploitation and the restocking of natural populations. Fourth, these tools offer the ability to advance aquaculture production by means of genomic selection for growth or disease resistance, and to identify wild populations with the most potential for domestication and breeding.

### Some Encouraging Progress

While much remains to be done for a full integration of genomics into management and policy decisions, it is encouraging that genomics is increasingly part of focused research programmes such as FishPopTrace [31] (https://fishpoptrace.jrc.ec.europa.eu/) or AquaTrace focusing on natural populations and farm escapees, respectively (https://aquatrace.eu/). In aquaculture, genomics is leading to rapid advancements in breeding programmes, and is necessary to fulfil food traceability requirements and industry regulation as well as risk assessments [45]. Moreover, the value of genetic and genomic information to ensure the sustainable exploitation of marine resources has found increased recognition. This is demonstrated by initiatives of international organisations such as Food and Agriculture Organization (FAO) (e.g., report in preparation by the Intergovernmental Technical Working Group on Aquatic Genetic Resources)

or the Marine Stewardship Council has established a programme of genetic testing of species/stocks in relation to food authenticity and compliance with eco-certification. The Organisation for Economic Co-operation and Development (OECD) has also made significant investment/profiling in harnessing the future of biotechnology (including genomics) in the exploitation and management of marine resources.

## Communication Is Key

To keep moving forward, there is a pressing need for concerted efforts that should focus on tight integration of genomic approaches to inform management and production practices. This can only be achieved by a clear definition and formulation of needs that require practical solutions (Ovenden and Moore, S11, Box 1). Arguably, the swift advancement of genomic research risks placing a focus on scientific progress thereby distracting from actual management needs and increasing the gap between scientists, managers and policy makers [46]. Accordingly, such integration can only be achieved if researchers focus more on the immediate needs and pay attention to guidelines and obligations in relevant legal and policy frameworks [46]. Fisheries scientists are not trained across all disciplines; like economic, politics, or social sciences, genetics is an area that is commonly neglected. At the same time, managers and policy makers are probably still largely unaware of the prospective usefulness of genomic tools for improved management, production, and food security. Efficient technology transfer will thus also depend on a closer communication between fisheries scientists, assessment experts, modellers, and geneticists in addition to better communication with managers and policy makers (Ovenden and Moore, S11). For example, a reference to genetics in the EU legislation was only rendered possible after extensive consultation between fisheries geneticists and policy makers (Martinsohn, S9). This highlights the need to improve and refine the communication between researchers and end-users, a conclusion that was also reached by Waples *et al*. [16] (Box 1). One way to achieve this is to have facilitators (e.g., social scientists) acting between researchers, managers, fishermen, and aquaculture producers, whose job is to facilitate communication by use of a common language [47]. Scientists willing to act as connectors between research providers and industry are necessary to achieve this and should be rewarded for their contribution. For instance, several agencies in the US, Canada, Australia, and the UK already employ geneticists to play such a role. Too often, however, academic institutions and grant providers are excessively focused on scientific output per se (e.g., publications), and overlook whether the research is translated and applied to tangible problems. By asking scientists to describe the potential impact of their research and by celebrating the results, institutions can achieve a change in attitude to what is perceived and valued as scientific achievement. This would facilitate scientists to become more proactive in trying to translate research outputs into practical solutions. Additionally, seafood genomics research tends to be exclusively published in scientific journals, which are sometimes neither readily available to government workers nor easily transferable into management applications. For these reasons, more focus on providing easy access to scientific publications to all stakeholders is important, for example, by publishing articles in open access journals. In addition, it is desirable to advocate reports by agency geneticists that would translate results into accessible language to non-specialists, as is already done in fisheries agencies in Australia and facilitated by funding bodies. By making genomics data accessible to researchers worldwide, a scientific dialogue is created that facilitates advancements of earlier work, underlining the central role of knowledge and innovation in generating scientific growth. Furthermore, communication also encourages collaboration and helps to avoid duplication of effort, and involves citizens and society, which together improve the transparency of the scientific process.

## Management Structures

Fisheries management is based on data and scientific advice, and control measures to ensure that rules are applied fairly to and complied with by all. The prevailing stagnation in integrating

genetic/genomic information into fisheries management schemes is in stark contrast to the current swift progress in genomics, and suggests that historical settings and political considerations may impede the integration of new scientific approaches, when defining policies and management strategies. Management structures must reflect the types of data that need to be evaluated. Consequently, relevant legal bodies and authorities need to bring together all stakeholders (management practitioners, policy makers, fisheries, and genomic scientists) to facilitate interaction and promote synergistic activities underpinning improved stock monitoring, prediction, and management to ensure sustainability. This change in structure also means that the traditional training of fisheries and aquaculture scientists need to be modernised, and should include a solid training in genetic/genomic applications, in addition to the more traditional teachings on aquatic ecology, population dynamics and catch quota management. The training should also include communication training, as part of the problem is often also the inability of many scientists to communicate clearly with the public, and professionals who are not trained in genetic/genomic approaches. Once a new cohort of trained fisheries and aquaculture scientists has been recruited, progress in the integration of genomic/genetic data to inform the management of capture fisheries and aquaculture practices can be expected.

## Concluding Remarks

There is now ample published evidence demonstrating the high value of genomics and genomic-derived information in helping to secure a sustainable future of seafood. Previous studies demonstrated the critical importance of maintaining population diversity for stabilizing ecosystem services and securing the economies and livelihoods that depend on them [48]. Moreover, a science-based integrated ecosystem approach necessitates innovative holistic monitoring to obtain data to determine the health of aquatic ecosystems and adjust management decisions accordingly [17]. When countries/regions make an effort to improve their management and monitoring practices, they largely achieve that. The corollary of this is that countries with the least-effective management systems have the greatest potential for improving long-term stock status outcomes and should be the focus of efforts to improve fisheries management globally [13]. Nowadays, many stocks are sustainably harvested or recovering [6] making it possible focus on maintaining seafood security by the innovative use of genomics.

In our opinion, there is no reason to further delay the application of genomic tools in fisheries management and aquaculture production. Instead, we need immediate involvement of all stakeholders, including science and management colleagues, to work together to remove structural roadblocks and to focus on ways that support integration of genomic informed methods into management and production practices. Indeed, genomics has much to offer towards this end as it can be applied to determine the health of aquatic ecosystems, to monitor the genetic composition of organisms and their adaptability, as well as the biological entities within the ecosystem around them. Moreover, new areas of inquiry will likely be addressed in the next years and add to the relevance of genomics for improved fisheries and aquaculture management (see Outstanding Questions). While we realise that compromises are inevitable within governance structures and present sociopolitical frameworks, we believe that, as for agricultural or medical professions, it would be negligent if society overlooked new scientific tools for safeguarding seafood and environmental security. It is our hope that the solutions proposed in this paper will help to pave the way forward and that genomic-informed data will become part of the standard data that is used to manage our precious seafood resources.

## Uncited Reference

[9].

## Outstanding Questions

Will genomics allow establishing clear links between genotype, phenotype, and fitness, and hence robustly ascertain the functional effects of observed genomic changes?

It is unlikely that we will understand the full genomic basis of any complex trait in a commercially harvested species within the next few years. However, an integrative approach should lead to substantial progress towards finding causal relationships among genome and epigenomic variation, gene expression, phenotypes, and the environment, to forecast the potential of species for adaptation adapting to changing environments.

What can we learn from a more comprehensive understanding of the genomic basis of fisheries-induced evolution?

A better understanding of how fisheries-induced evolution impacts populations at the genomic level can provide fundamentally new insights about into how it operates mechanistically and to what extent it is detrimental for the future productivity of fish populations.

How can we distinguish direct genomic targets of selection (resulting either from domestication in aquaculture, selective harvesting or global environmental change) from loci in other genomic regions that are indirectly affected through genetic correlations?

Studying the response to the same selection pressure in multiple different populations may help to narrow in on the particular targets because favoured variants may exist on different genomic backgrounds so that direct effects of selection should cause parallel allele frequency shifts, whereas hitch-hiking effects should not necessarily cause parallel changes.

How will the integration of genomic, cellular, and organismal-level assessments of cultured species help discerning the pathogenic potential and biosecurity risks of microbial communities?

Merging host gene expression profiling, histopathology and pathogen monitoring will allow identifying disease phenotypes in cultured species

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## Supplemental Information

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